

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/001,737DATE: 10/06/98  
TIME: 15:05:39

INPUT SET: S28966.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

ENTERED

## SEQUENCE LISTING

1  
2  
3 (1) General Information:  
4  
5 (i) APPLICANTS: Mizzen, Lee  
6 Wisniewski, Jan  
7  
8 (ii) TITLE OF INVENTION: STREPTOCACCAL HEAT SHOCK PROTEINS OF THE  
9 HSP60 FAMILY  
10  
11 (iii) NUMBER OF SEQUENCES: 91  
12  
13 (iv) CORRESPONDENCE ADDRESS:  
14 (A) ADDRESSEE: SEED and BERRY LLP  
15 (B) STREET: 701 Fifth Avenue, 6300 Columbia Center  
16 (C) CITY: Seattle  
17 (D) STATE: Washington  
18 (E) COUNTRY: USA  
19 (F) ZIP: 98104  
20  
21 (v) COMPUTER READABLE FORM:  
22 (A) MEDIUM TYPE: Floppy disk  
23 (B) COMPUTER: IBM PC compatible  
24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS  
25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30  
26  
27 (vi) CURRENT APPLICATION DATA:  
28 (A) APPLICATION NUMBER: US 09/001,737  
29 (B) FILING DATE: 31-DEC-1997  
30 (C) CLASSIFICATION:  
31  
32 (viii) ATTORNEY/AGENT INFORMATION:  
33 (A) NAME: Sharkey, Richard G.  
34 (B) REGISTRATION NUMBER: 32,629  
35 (C) REFERENCE/DOCKET NUMBER: 870109.408  
36  
37 (ix) TELECOMMUNICATION INFORMATION:  
38 (A) TELEPHONE: (206) 622-4900  
39 (B) TELEFAX: (206) 682-6031  
40  
41  
42 (2) INFORMATION FOR SEQ ID NO:1:  
43  
44 (i) SEQUENCE CHARACTERISTICS:  
45 (A) LENGTH: 1665 base pairs  
46 (B) TYPE: nucleic acid

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47      (C) STRANDEDNESS: single
48      (D) TOPOLOGY: linear
49
50
51
52      (ix) FEATURE:
53          (A) NAME/KEY: CDS
54          (B) LOCATION: 15..1649
55
56
57      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58
59      GAATTCGGCT TCAT ATG GCG GCT AAA GAC GTA AAA TTC GGT AAC GAC GCT      50
60          Met Ala Ala Lys Asp Val Lys Phe Gly Asn Asp Ala
61              1              5              10
62
63      CGT GTG AAA ATG CTG CGC GGC GTA AAC GTA CTG GCA GAT GCA GTG AAA      98
64      Arg Val Lys Met Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys
65          15              20              25
66
67      GTT ACC CTC GGC CCA AAA GGC CGT AAC GTA GTT CTG GAT AAA TCT TTC      146
68      Val Thr Leu Gly Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe
69          30              35              40
70
71      GGT GCA CCG ACC ATC ACT AAA GAT GGT GTT TCC GTA GCA CGT GAA ATC      194
72      Gly Ala Pro Thr Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile
73          45              50              55              60
74
75      GAA CTG GAA GAC AAG TTC GAA AAC ATG GGT GCG CAG ATG GTG AAA GAA      242
76      Glu Leu Glu Asp Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu
77          65              70              75
78
79      GTT GCC TCT AAA GCG AAC GAC GCT GCA GGT GAC GGT ACC ACC ACC GCA      290
80      Val Ala Ser Lys Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala
81          80              85              90
82
83      ACC GTA CTG GCT CAG TCC ATC ATC ACT GAA GGC CTG AAA GCC GTT GCT      338
84      Thr Val Leu Ala Gln Ser Ile Ile Thr Glu Gly Leu Lys Ala Val Ala
85          95              100              105
86
87      GCG GGC ATG AAC CCG ATG GAT CTG AAA CGT GGT ATC GAC AAA GCT GTC      386
88      Ala Gly Met Asn Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val
89          110              115              120
90
91      GCT GCT GCT GTT GAA GAA CTG AAA GCA CTG TCC GTA CCG TGC TCC GAC      434
92      Ala Ala Ala Val Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp
93          125              130              135              140
94
95      TCT AAA GCT ATT GCT CAG GTT GGT ACC ATC TCC GCT AAC TCC GAC GAA      482
96      Ser Lys Ala Ile Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu
97          145              150              155
98
99      ACC GTA GGT AAA CTG ATC GCT GAA GCG ATG GAC AAA GTC GGT AAA GAA      530

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100	Thr	Val	Gly	Lys	Leu	Ile	Ala	Glu	Ala	Met	Asp	Lys	Val	Gly	Lys	Glu	
101				160					165					170			
102																	
103	GGC	GTG	ATC	ACC	GTT	GAA	GAC	GGT	ACC	GGT	CTG	CAG	GAC	GAA	CTG	GAC	578
104	Gly	Val	Ile	Thr	Val	Glu	Asp	Gly	Thr	Gly	Leu	Gln	Asp	Glu	Leu	Asp	
105			175					180					185				
106																	
107	GTG	GTT	GAA	GGT	ATG	CAG	TTC	GAC	CGT	GGC	TAC	CTG	TCT	CCT	TAC	TTC	626
108	Val	Val	Glu	Gly	Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Pro	Tyr	Phe	
109		190					195					200					
110																	
111	ATC	AAC	AAG	CCG	GAA	ACT	GGC	GCA	GTA	GAA	TTG	GAA	AGC	CCG	TTC	ATC	674
112	Ile	Asn	Lys	Pro	Glu	Thr	Gly	Ala	Val	Glu	Leu	Glu	Ser	Pro	Phe	Ile	
113	205					210					215					220	
114																	
115	CTG	CTG	GCT	GAC	AAG	AAA	ATC	TCC	AAC	ATC	CGC	GAA	ATG	CTG	CCG	GTT	722
116	Leu	Leu	Ala	Asp	Lys	Lys	Ile	Ser	Asn	Ile	Arg	Glu	Met	Leu	Pro	Val	
117					225					230					235		
118																	
119	CTG	GAA	GCT	GTA	GCG	AAA	GCA	GGC	AAA	CCG	CTG	CTG	ATC	ATC	GCT	GAA	770
120	Leu	Glu	Ala	Val	Ala	Lys	Ala	Gly	Lys	Pro	Leu	Leu	Ile	Ile	Ala	Glu	
121				240						245					250		
122																	
123	GAT	GTT	GAA	GGC	GAA	GCG	CTG	GCA	ACT	CTG	GTT	GTT	AAC	ACC	ATG	CGC	818
124	Asp	Val	Glu	Gly	Glu	Ala	Leu	Ala	Thr	Leu	Val	Val	Asn	Thr	Met	Arg	
125			255					260					265				
126																	
127	GGT	ATC	GTA	AAA	GTC	GCT	GCG	GTT	AAA	GCA	CCT	GGC	TTC	GGC	GAT	CGT	866
128	Gly	Ile	Val	Lys	Val	Ala	Ala	Val	Lys	Ala	Pro	Gly	Phe	Gly	Asp	Arg	
129		270					275					280					
130																	
131	CGT	AAA	GCA	ATG	CTG	CAG	GAT	ATC	GCT	ACC	CTG	ACC	GGT	GGT	ACC	GTT	914
132	Arg	Lys	Ala	Met	Leu	Gln	Asp	Ile	Ala	Thr	Leu	Thr	Gly	Gly	Thr	Val	
133	285					290					295					300	
134																	
135	ATC	TCT	GAA	GAG	ATC	GGT	ATG	GAG	CTG	GAA	AAA	GCA	ACT	CTG	GAA	GAT	962
136	Ile	Ser	Glu	Glu	Ile	Gly	Met	Glu	Leu	Glu	Lys	Ala	Thr	Leu	Glu	Asp	
137					305					310					315		
138																	
139	CTG	GGC	CAG	GCG	AAA	CGC	GTT	GTT	ATC	AAC	AAA	GAT	ACC	ACC	ACC	ATC	1010
140	Leu	Gly	Gln	Ala	Lys	Arg	Val	Val	Ile	Asn	Lys	Asp	Thr	Thr	Thr	Ile	
141				320					325						330		
142																	
143	ATC	GAT	GGC	GTG	GGC	GAC	GAA	GCT	GCA	ATC	CAG	GGT	CGC	GTG	ACT	CAG	1058
144	Ile	Asp	Gly	Val	Gly	Asp	Glu	Ala	Ala	Ile	Gln	Gly	Arg	Val	Thr	Gln	
145			335					340					345				
146																	
147	ATT	CGT	CAG	CAG	ATC	GAA	GAA	GCA	ACT	TCC	GAC	TAT	GAC	CGT	GAA	AAA	1106
148	Ile	Arg	Gln	Gln	Ile	Glu	Glu	Ala	Thr	Ser	Asp	Tyr	Asp	Arg	Glu	Lys	
149		350					355					360					
150																	
151	CTG	CAG	GAG	CGC	GTA	GCG	AAA	CTG	GCA	GGC	GGC	GTT	GCG	GTT	ATC	AAA	1154
152	Leu	Gln	Glu	Arg	Val	Ala	Lys	Leu	Ala	Gly	Gly	Val	Ala	Val	Ile	Lys	

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153	365		370		375		380	
154								
155	GTT GGT GCT GCG ACT GAA GTT GAA ATG AAA GAG AAG AAA GCC CGC GTT							1202
156	Val Gly Ala Ala Thr Glu Val Glu Met Lys Glu Lys Lys Ala Arg Val							
157		385		390			395	
158								
159	GAA GAT GCC CTG CAC GCT ACC CGT GCT GCG GTA GAA GAA GGC GTG GTT							1250
160	Glu Asp Ala Leu His Ala Thr Arg Ala Ala Val Glu Glu Gly Val Val							
161		400		405			410	
162								
163	GCT GGT GGT GGC GTT GCG CTG ATT CGC GTA GCG TCT AAA ATT GCC GGC							1298
164	Ala Gly Gly Gly Val Ala Leu Ile Arg Val Ala Ser Lys Ile Ala Gly							
165		415		420			425	
166								
167	CTG AAA GGT CAG AAC GAA GAC CAG AAC GTA GGT ATC AAA GTT GCG CTG							1346
168	Leu Lys Gly Gln Asn Glu Asp Gln Asn Val Gly Ile Lys Val Ala Leu							
169		430		435			440	
170								
171	CGC GCA ATG GAA TCC CCA CTG CGT CAA ATC GTA CTG AAC TGC GGC GAA							1394
172	Arg Ala Met Glu Ser Pro Leu Arg Gln Ile Val Leu Asn Cys Gly Glu							
173		445		450			455	460
174								
175	GAG CCG TCT GTA GTG GCT AAC ACC GTG AAA GCC GGT GAC GGT AAC TAC							1442
176	Glu Pro Ser Val Val Ala Asn Thr Val Lys Ala Gly Asp Gly Asn Tyr							
177		465		470			475	
178								
179	GGT TAC AAC GCT GCA ACT GAA GAA TAC GGC AAC ATG ATC GAC ATG GGT							1490
180	Gly Tyr Asn Ala Ala Thr Glu Glu Tyr Gly Asn Met Ile Asp Met Gly							
181		480		485			490	
182								
183	ATC CTG GAT CCA ACC AAA GTA ACT CGT TCT GCT CTG CAG TAC GCG GCT							1538
184	Ile Leu Asp Pro Thr Lys Val Thr Arg Ser Ala Leu Gln Tyr Ala Ala							
185		495		500			505	
186								
187	TCT GTT GCG GGT CTG ATG ATC ACC ACC GAG TGC ATG GTT ACC GAC CTG							1586
188	Ser Val Ala Gly Leu Met Ile Thr Thr Glu Cys Met Val Thr Asp Leu							
189		510		515			520	
190								
191	CCG AAA GGC GAT GCA CCT GAC TTA GGT GCT GCT GGT GGT ATG GGC GGC							1634
192	Pro Lys Gly Asp Ala Pro Asp Leu Gly Ala Ala Gly Gly Met Gly Gly							
193		525		530			535	540
194								
195	ATG GGC GGA ATG ATG TGATCAAGCC GAATTC							1665
196	Met Gly Gly Met Met							
197		545						
198								
199								
200	(2) INFORMATION FOR SEQ ID NO:2:							
201								
202	(i) SEQUENCE CHARACTERISTICS:							
203	(A) LENGTH: 545 amino acids							
204	(B) TYPE: amino acid							
205	(D) TOPOLOGY: linear							

# RAW SEQUENCE LISTING PATENT APPLICATION *US/09/001,737*

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*INPUT SET: S28966.raw*

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206
207      (ii) MOLECULE TYPE: protein
208
209      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
210
211 Met Ala Ala Lys Asp Val Lys Phe Gly Asn Asp Ala Arg Val Lys Met
212   1              5              10              15
213
214 Leu Arg Gly Val Asn Val Leu Ala Asp Ala Val Lys Val Thr Leu Gly
215           20              25              30
216
217 Pro Lys Gly Arg Asn Val Val Leu Asp Lys Ser Phe Gly Ala Pro Thr
218           35              40              45
219
220 Ile Thr Lys Asp Gly Val Ser Val Ala Arg Glu Ile Glu Leu Glu Asp
221   50              55              60
222
223 Lys Phe Glu Asn Met Gly Ala Gln Met Val Lys Glu Val Ala Ser Lys
224   65              70              75              80
225
226 Ala Asn Asp Ala Ala Gly Asp Gly Thr Thr Thr Ala Thr Val Leu Ala
227           85              90              95
228
229 Gln Ser Ile Ile Thr Glu Gly Leu Lys Ala Val Ala Ala Gly Met Asn
230           100             105             110
231
232 Pro Met Asp Leu Lys Arg Gly Ile Asp Lys Ala Val Ala Ala Ala Val
233           115             120             125
234
235 Glu Glu Leu Lys Ala Leu Ser Val Pro Cys Ser Asp Ser Lys Ala Ile
236           130             135             140
237
238 Ala Gln Val Gly Thr Ile Ser Ala Asn Ser Asp Glu Thr Val Gly Lys
239           145             150             155             160
240
241 Leu Ile Ala Glu Ala Met Asp Lys Val Gly Lys Glu Gly Val Ile Thr
242           165             170             175
243
244 Val Glu Asp Gly Thr Gly Leu Gln Asp Glu Leu Asp Val Val Glu Gly
245           180             185             190
246
247 Met Gln Phe Asp Arg Gly Tyr Leu Ser Pro Tyr Phe Ile Asn Lys Pro
248           195             200             205
249
250 Glu Thr Gly Ala Val Glu Leu Glu Ser Pro Phe Ile Leu Leu Ala Asp
251           210             215             220
252
253 Lys Lys Ile Ser Asn Ile Arg Glu Met Leu Pro Val Leu Glu Ala Val
254           225             230             235             240
255
256 Ala Lys Ala Gly Lys Pro Leu Leu Ile Ile Ala Glu Asp Val Glu Gly
257           245             250             255
258

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**SEQUENCE VERIFICATION REPORT**  
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***INPUT SET: S28966.raw***

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